Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

1.-14. (Canceled)

15. (Currently amended) A method for identifying an agent that interacts with P-selectin LE, comprising the steps of:

providing a crystal comprising a P-selectin LE, wherein the P-selectin LE comprises an amino acid sequence of SEQ ID NO:6, SEQ ID NO:8 or SEQ ID NO:9, or conservative substitutions thereof;

obtaining the relative structural coordinates of the crystallized P-selectin LE;

generating a three dimensional model of P-selectin LE using the relative structural coordinates according to Figures 2, 3 or 5, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å; and

employing said three-dimensional model to design or select an agent that interacts with P-selectin LE, thereby identifying the agent.

16. (Previously presented) The method of Claim 15, further comprising the steps of:

obtaining the identified agent; and

contacting the identified agent with P-selectin LE in order to determine the effect the agent has on P-selectin LE activity.

17.-35. (Canceled)

36. (Previously presented) The method of claim 15, wherein the agent is selected or designed by performing computer fitting analysis of the agent with the three dimensional model.

37. (Previously presented) The method of claim 16, wherein obtaining the agent comprises synthesizing the agent.

38. (Previously presented) The method of claim 15, wherein the agent is selected or designed to interact with an active site of P-selectin LE.

39. (Previously presented) The method of claim 15, wherein the agent is selected or designed to interact with an active site of P-selectin LE, and wherein the active site comprises the relative structural coordinates of amino acids TYR48, GLU80, ASN82, GLU92, TYR94, PRO98, SER99, ASN105, ASP106, and GLU107 and bound calcium according to Figure 3, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.

40. (Previously presented) The method of claim 39, wherein the active site further comprises the relative structural coordinates of amino acid residues TYR44, SER46, SER47, ALA77, ASP78, ASN79, PRO81, ASN83, ARG85, GLU88, CYS90, ILE93, LYS96, SER97, ALA100, TRP104, HIS108, LYS111, and LYS113 according to Figure 3, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.

41. (Previously presented) The method of claim 15, wherein the agent is selected or designed to interact with an active site of P-selectin LE, and wherein the active site comprises the relative structural coordinates of amino acid residues ALA9, TYR45, SER46, SER47, TYR48, GLU80, ASN82, LYS84, ARG85, GLU88, GLU92, TYR94, PRO98, SER99, ASN105, ASP106, GLU107, HIS108, LEU110, LYS111, LYS112, LYS113, HIS114 and bound strontium according to Figure 5, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.

42. (Previously presented) The method of claim 41, wherein the active site further comprises the relative structural coordinates of amino acid residues SER6, THR7, LYS8, TYR10, SER11, TYR44, TYR49, TRP50, ALA77, ASP78, ASN79, PRO81, ASN83, ASN86,

ASN87, CYS90, ILE93, ILE95, LYS96, SER97, ALA100, TRP104, and CYS109 according to Figure 5, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.

43. (Previously presented) The method of claim 15, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

44. (Previously presented) The method of claim 15, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

45. (Previously presented) The method of claim 39, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

46. (Previously presented) The method of claim 39, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

47. (Previously presented) The method of claim 40, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

48. (Previously presented) The method of claim 40, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

49. (Previously presented) The method of claim 41, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

50. (Previously presented) The method of claim 41, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

51. (Previously presented) The method of claim 42, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

52. (Previously presented) The method of claim 42, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

53. (Previously presented) The method of claim 15, wherein the three dimensional model is generated using the relative structural coordinates according to Figure 2, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

54. (Previously presented) The method of claim 15, wherein the three dimensional model is generated using the relative structural coordinates according to Figure 3, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

55. (Previously presented) The method of claim 15, wherein the three dimensional model is generated using the relative structural coordinates according to Figure 5, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

56. (Currently amended) A method for identifying an agent that interacts with P-selectin LE, comprising the steps of:

providing a crystal comprising a P-selectin LE, wherein the P-selectin LE comprises an amino acid sequence of SEQ ID NO:6, SEQ ID NO:8 or SEQ ID NO:9, or conservative substitutions thereof;

obtaining the relative structural coordinates of the crystallized P-selectin LE;

generating a three dimensional model of P-selectin LE using the relative structural coordinates according to Figures 2, 3 or 5 ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å;

employing said three-dimensional model to design or select an agent that interacts with P-selectin LE;

obtaining the designed or selected agent; and

contacting the designed or selected agent with P-selectin LE in order to determine the effect the agent has on P-selectin LE activity.

57. (Previously presented) The method of claim 56, wherein obtaining the agent comprises synthesizing the agent.

58. (Previously presented) The method of claim 56, wherein the three dimensional model is generated using the relative structural coordinates according to Figure 2, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

59. (Previously presented) The method of claim 56, wherein the three dimensional model is generated using the relative structural coordinates according to Figure 3, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

60. (Previously presented) The method of claim 56, wherein the three dimensional model is generated using the relative structural coordinates according to Figure 5, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

61. (New) The method of claim 15 or 56, wherein the P-selectin LE crystal has space group $P2_1$ with unit cell parameters of a=81.0 Å, b=60.8Å, c=91.4Å, and beta=103.6°.

62. (New) The method of claim 15 or 56, wherein the P-selectin LE in the crystal is complexed with SLe^x.

63. (New) The method of claim 62, wherein the crystal has space group $P2_1$ with unit cell parameters of a=81.1 Å, b=60.5Å, c=91.4Å, and beta=103.3°.

64. (New) The method of claim 15 or 56, wherein the P-selectin LE in the crystal is complexed with a PSGL-1 peptide.

65. (New) The method of claim 64, wherein the crystal has space group I222 with unit cell parameters of a=63.4Å, b=96.8Å, and c=187.3Å.

66. (New) A method for identifying an agent that interacts with P-selectin LE, comprising:

providing relative structural coordinates of a P-selectin LE which comprises an amino acid sequence of SEQ ID NO:6, SEQ ID NO:8 or SEQ ID NO:9, or conservative substitutions thereof, wherein the relative structural coordinates of P-selectin LE are selected from the group consisting of:

(i) the relative structural coordinates according to Figure 2, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å;

(ii) the relative structural coordinates of amino acids TYR44, SER46, SER47, TYR48, ALA77, ASP78, ASN79, GLU80, PRO81, ASN82, ASN83, ARG85, GLU88, CYS90, GLU92, ILE93, TYR94, LYS96, SER97, PRO98, SER99, ALA100, TRP104, ASN105, ASP106, GLU107, HIS108, LYS111, and LYS113 according to Figure 3, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å; and

(iii) the relative structural coordinates of amino acids SER6, THR7, LYS8, ALA9, TYR10, SER11, TYR44, TYR45, SER46, SER47, TYR48, TYR49, TRP50, ALA77, ASP78, ASN79, GLU80, PRO81, ASN82, ASN83, LYS84, ARG85, ASN86, ASN87, GLU88, CYS90, GLU92, ILE93, TYR94, ILE95, LYS96, SER97, PRO98, SER99, ALA100, TRP104, ASN105, ASP106, GLU107, HIS108, CYS109, LEU110, LYS111, LYS112, LYS113, and HIS114 according to Figure 5, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å;;

generating a three-dimensional model of P-selecting LE using the relative structural coordinates of P-selectin LE;

employing said three-dimensional model to design or select an agent that interacts with P-selectin LE; and

contacting the designed or selected agent with P-selectin LE in order to determine the effect the agent has on P-selectin LE activity, thereby identifying the agent.

67. (New) The method of claim 66, wherein the relative structural coordinates comprise the coordinates according to Figure 2, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.

68. (New) The method of claim 66, wherein the relative structural coordinates comprise the coordinates according to Figure 3, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.

69. (New) The method of claim 66, wherein the relative structural coordinates comprise the coordinates according to Figure 5, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.